

REMARKS

The Office Action mailed November 6, 2002 has been received and reviewed. Claims 1-23 are currently pending in the application and all claims stand rejected. Claims 5, 7 and 22 have been withdrawn from consideration as assertedly being drawn to a non-elected invention. Claims 1-6, 8-21 and 23 have been amended and new claims 24-31 have been added as set forth herein. All amendments are made without prejudice or disclaimer. Reconsideration is respectfully requested.

Objection to Specification

The specification was objected to for not containing an abstract of the disclosure and for including an embedded hyperlink. The specification has been amended to include an "ABSTRACT" and to remove the embedded hyperlink. Withdrawal of the objections is thus requested.

Sequence Listing

It was thought to be unclear where the Start (atg) and Stop (tag, taa, or tga) codons of SEQ ID NOS: 1 and 3 are located and that clarification is required. Applicants respectfully submit that the sequence rules do not require the location of start and stop codons to be identified. (*See*, 37 C.F.R. §§ 1.821-1.825). Withdrawal of the objection is thus requested.

Objections to Claims

Claim 23 was objected to for reading on non-elected material. The phrase "or anti-sense" has been removed from claim 23. Withdrawal of the objection is thus requested.

Claims 14-18 were objected under 37 CFR 1.75(c) as being in improper dependent form since that a multiple dependent claim depended on a multiple dependent claim. The phrase "or Claim 13" has been deleted from claims 14-18. Withdrawal of the objections is requested.

Rejections under 35 U.S.C. § 112, second paragraph

Claims 1-4, 6, 8-11, 14-19, 21 and 23 were rejected under 35 U.S.C. § 112, second paragraph, as assertedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicants regard as the invention. At least partially in view of the amendments to claims 1-4, 6, 8-11, 14-19, 21 and 23, applicants respectfully request withdrawal of the rejections.

Regarding claims 1 and 2, the words "an" and "molecule" have been inserted in accordance with the suggestion of the Examiner.

With regard to the phrase "substantially homologous" in claim 1 and other claims, it is defined in the specification as "substantially homologous DNA sequences from plants encoding proteins with deduced amino acid sequences of 25% of greater identify, and 40% or greater similarity." (Specification, page 4, lines 14-16.) Since "substantially homologous" has a definite meaning as defined in the specification, the phrase should be considered definite.

With regard to claims 3 and 4, the term "contains" has been inserted in accordance with the suggestion of the Examiner.

In claim 6, the word "A" has been replaced with "The" as suggested by the Examiner.

Regarding claims 8 and 9, the parentheses have been deleted and the phrase "having accession number" has been inserted in accordance with the Examiner's suggestion.

Regarding claims 9 and 10, the first "or" has been deleted as suggested by the Examiner.

The phrase "an introduced" has been inserted into claims 10 and 11 as suggested by the Examiner to clarify that the sequences are introduced into the plant and seed.

With regard to claims 14-18, the term "genomically-unmodified" has been replaced with the term "untransformed." As stated in the specification, "plants or seeds according to the invention are best compared with results from averages of statistically-significant numbers of untransformed (control) plants or seeds of the same genotype grown under identical conditions at the same time." (*Id.* at page 5, lines 21-24). Accordingly, the claims should be considered definite.

With further regard to claims 14-18, "A" has been replaced by "The" in accordance with the suggestions of the Examiner.

Turning to claim 21, it is definite as written since the information provided in parenthesis is an alternative way of referring to the listed plant and does not constitute a further limitation. The claim has also been amended to recite "other members of the plant family *Gramineae* not listed" for clarification. Accordingly, claim 21 should be considered definite.

In claim 23, the term "proportions" has been replaced with the term "ratio" to clarify that the "/" is used to denote the ratio of diacylglycerol to triacylglycerol.

With further regard to claim 23, it was thought that the meaning of "changing" should be stated as "increases" or "decreases." Applicants respectfully submit the term "changing" is definite and supported by the as-filed specification since the oil content may be increased (*See, Id.* at page 7, lines 29-30) while the ratio of diacylglycerol to triacylglycerol may be decreased. (*See, e.g., Id.* at FIG. 1, increasing DGAT production would convert diacylglycerol to triacylglycerol and, thus, decrease the ratio).

Also with regard to claim 23, it was thought that essential steps were missing. Although applicants do not agree that claim 23 is indefinite since the term "comprising is inclusive or open-ended and does not exclude, additional, unrecited elements or method steps," (M.P.E.P. § 2111.03) for the sake of expedited prosecution the phrase "expressing the nucleic acid sequence" has been added to claim 23 to comply with the suggestion of the Examiner.

In view of the amendments and remarks presented herein, applicants respectfully request reconsideration and withdrawal of the indefinite rejections of claims 1-4, 6, 8-11, 14-19, 21 and 23.

Rejections under 35 U.S.C. § 101

Claims 10 and 11

Claims 10 and 11 were rejected under 35 U.S.C. § 101 as assertedly being directed to non-statutory subject matter. Applicants respectfully traverse the rejections as hereinafter set forth.

Specifically, it was asserted that the "hand of man" was not involved in the invention since SEQ ID NO: 1 is inherently possessed by naturally occurring *Arabidopsis*.

Claims 10 and 11 have been amended to include the phrase "an introduced" preceding the phrases "a part of SEQ ID NO: 1" and a "sequence that is substantially homologous to SEQ ID NO: 1." Since the "hand of man" was used to introduce the nucleotide sequences, withdrawal of the rejections of claims 10 and 11 is requested.

Claims 1-4, 6, 10-21 and 23

Claims 1-4, 6, 10-21 and 23 were rejected under 35 U.S.C. § 101 as assertedly not being supported by an asserted or a well established utility. Applicants respectfully traverse the rejections as hereinafter set forth.

It was asserted that the phrase "or a part of SEQ ID NO:1 or 3" can be interpreted as meaning one base pair and that since the applicant has not disclosed a utility for one base pair, a specific asserted utility or a well established utility has not been established.

Independent claims 1-4, 10, 11 and 23 have been amended such that the nucleic acid molecule corresponds to a polypeptide having diacylglycerol acyltransferase activity. The claims have also been amended such that the part of SEQ ID NO: 1 or 3 is a functional part. Accordingly, the claims require a functional part of SEQ ID NO: 1 or 3 corresponding to a polypeptide having diacylglycerol acyltransferase activity which is demonstrated in the specification to have utility. (*See, Id.* at page 24 under heading "Over-Expression of the DGAT cDNA in Wild-Type *A. Thaliana*").

It was further asserted that neither a demonstrated utility nor a well-known utility was shown for SEQ ID NO: 3. Specifically, it was asserted that the applicants have not shown that SEQ ID NO: 3 encodes a protein having acyltransferase activity, why the protein encoded by SEQ ID NO: 3 is twenty two amino acids less than the protein encoded by the cDNA of SEQ ID NO: 1 or whether the protein encoded by SEQ ID NO: 3 contains the catalytic domains essential for acyltransferase activity.

As disclosed in the summary of the listed sequences and the sequence listing, SEQ ID NO: 3 is a vector which includes the DNA sequence of ATCC no PTA-988 which includes the *Arabidopsis* DGAT gene. (*See, Id.* at page 33, 36; *See also, Sequence Listing*, page 4). SEQ ID NO: 3 differs from SEQ ID NO: 1 in that SEQ ID NO: 3 is derived from the *Arabidopsis*

genomic DGAT gene, wherein SEQ ID NO: 1 is derived from *Arabidopsis* DGAT cDNA. Thus, SEQ ID NO: 3 includes the gene corresponding to a polypeptide having diacylglycerol acyltransferase activity. Using known cloning techniques and the sequence information contained within SEQ ID NO: 3, one of skill in the art would be able to clone the gene corresponding to a polypeptide having DGAT activity of SEQ ID NO: 3 into a vector such that the gene could be expressed without undue experimentation. Further, since the inventors have isolated SEQ ID NO: 3 and shown a utility for the gene contained therein, SEQ ID NO: 3 has utility.

In view of the amendments and remarks presented herein, reconsideration and withdrawal of the utility rejections of the claims are requested.

Rejections under 35 U.S.C. § 112, first paragraph

Utility

Claims 1-4, 6, 10-21 and 23 were rejected under 35 U.S.C. § 112, first paragraph, since it was asserted that the claimed invention was not supported by either a specific or a well established utility. Applicants respectfully traverse the rejections as hereinafter set forth.

As established with regard to the utility rejections, the claimed sequences are directed to nucleic acids corresponding to a polypeptide having diacylglycerol acyltransferase activity. Further, the applicants have shown a utility for nucleic acids corresponding to a polypeptide having diacylglycerol acyltransferase activity. (*See, Id.* at page 24 under the heading "Over-Expression of the DGAT cDNA in Wild-Type *A. Thaliana*"). Accordingly, reconsideration and withdrawal of the utility rejections of claims 1-4, 6, 10-21 and 23 are requested.

Enablement

Claims 1-4, 6, 10-21 and 23 were further rejected under 35 U.S.C. § 112, first paragraph, as assertedly lacking enablement for claims broadly drawn to an isolated DNA molecule comprising a part of SEQ ID NO: 1 or 3, or a sequence substantially homologous to SEQ ID NO: 1 or 3, wherein the claimed subject matter exhibits an altered seed oil content, an altered diacylglycerol content, an altered fatty acyl composition or an enhanced biomass. It was further

asserted that the given the unpredictability in the art and the undue breadth of the claims, that it would require undue experimentation by one skilled in the art to make and/or use the claimed invention. Applicants respectfully traverse the rejections as hereinafter set forth.

As set forth in the Office Action "the specification [is] enabling for claims limited to a DGAT cDNA clone of SEQ ID NO: 1 from *Arabidopsis* transformed into wild-type *Arabidopsis* to yield plants with an increased oil content" *inter alia*. Thus, the specification is enabling for SEQ ID NO: 1.

SEQ ID NO: 3 includes a gene corresponding to a polypeptide having diacylglycerol acyltransferase activity. As disclosed in the specification, SEQ ID NO: 3 is pgenomic DGAT including ATCC no PTA-988, which includes the *Arabidopsis* DGAT gene. (*See, Id.* at page 33 and 36). SEQ ID NO: 3 is enabled since one skilled in the art would be able to clone SEQ ID NO: 3, a part of SEQ ID NO: 3 or a sequence substantially homologous to SEQ ID NO: 3 using the sequence information contained within SEQ ID NO: 3 and known cloning techniques without undue experimentation. For instance, one skilled in the art would be able to design primers or use restriction enzymes using the sequence information of SEQ ID NO: 3 to clone the gene contained therein.

Regarding a part of SEQ ID NO: 1 or SEQ ID NO: 3, the functional part should be enabled as defined in the amended claims. As amended, the claims are directed to a nucleic acid molecule corresponding to a polypeptide having diacylglycerol acyltransferase activity, wherein the nucleic acid molecule contains a functional part of SEQ ID NO: 1 or 3. Thus, the amended claims are not directed to any part of SEQ ID NO: 1 or 3, but rather to a functional part of SEQ ID NO: 1 or 3 corresponding to a polypeptide with DGAT activity. Further, since SEQ ID NO: 1 is 1904 nucleotides in length and SEQ ID NO: 3 is 5193 nucleotides in length (*See, Sequence Listing*, pages 1 and 4) and the open reading frame of TAG1 cDNA corresponds to a polypeptide of 520 amino acids, which requires about 1560 nucleotides, (*See, Id.* at page 19, lines 13-15), it stands to reason that a functional part of SEQ ID NO: 1 or 3 (*e.g.*, at least the 1560 nucleotides) would be enabled.

Turning now to the limitation of a sequence substantially homologous to SEQ ID NO: 1 or 3, it is also enabled. As defined in the specification, "substantially homologous" DNA

sequences include "DNA sequences from plants encoding proteins with deduced amino acid sequences of 25% or greater identity, and 40% or greater similarity." (*Id.* at page 4, lines 14-16). Further, since small changes of the nucleotides in gene sequences may result in a reduced or enhanced effect of the gene, the sequence with the small change may function in the same manner as the full length gene. Also, since methods used to vary or shorten gene sequences are well known, homologues of gene sequences including the recited function are meant to be included within the scope of the present invention.

Claims 8 and 9 were further rejected under 35 U.S.C. § 112, first paragraph, as lacking enablement. Specifically, it was thought that since the plasmids are not readily obtainable or available, the deposit rules were not satisfied. Applicants respectfully traverse the rejections as hereinafter set forth.

Attached hereto is a copy of a deposit receipt from the ATCC evidencing deposit of plasmid pDGATcDNA and plasmid pDGATgene, PTA-988 and PTA-989, respectively, with the ATCC in accordance with the Budapest Treaty. As stated in the M.P.E.P. "once deposited in a depository complying with these regulations, a biological material will be considered to be readily available." (M.P.E.P. § 2404, *citing* 37 C.F.R. § 1.802(b)). Further, the ATCC is listed in the M.P.E.P. as an acceptable International Depositary Authority. (*See, M.P.E.P.* § 2405). In view of the deposit receipt from the ATCC, reconsideration and withdrawal of the enablement rejections of claims 8 and 9 are respectfully requested.

Written Description

Claims 1-4, 6, 10-21 and 23 were also rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way to reasonably convey to one skilled in the relevant art that the inventor has possession of the claimed invention at the time the application was filed.

Specifically, it was asserted that since the claims are directed to sequences "comprising" SEQ ID NO: 1 or 3, that the applicant did not indicate which base position of SEQ ID NO: 1 encodes the first amino acid or the last amino acid of the protein sequence and that one skilled in

the art would not be able to predictably determine the complete gene sequence containing SEQ ID NO: 1. Applicants respectfully traverse the rejections as hereinafter set forth.

As amended, the claims are directed to nucleic acids corresponding to a polypeptide having diacylglycerol acyltransferase activity. The specification discloses amplifying a full-length DGAT cDNA by using PCR with specified primers to introduce restriction sites on each end of the sequence. The resultant product was ligated into a vector which includes a promoter and a terminator sequence, such that the DGAT gene was under the control of the promoter of the vector and expressed. (*See, Id.* at page 23, lines 15-26). Further, one of skill in the art would be able to determine the reading frame of the claimed sequences without undue experimentation. Thus, the written description requirement is satisfied.

Additionally, it was thought that the applicants did not disclose which sequences are "substantially homologous" to SEQ ID NO: 1 or 3 with any certainty or predictability. Applicants respectfully traverse the rejection as hereinafter set forth.

As defined in the specification "substantially homologous" DNA sequences include "DNA sequences from plants encoding proteins with deduced amino acid sequences of 25% or greater identity, and 40% or greater similarity." (*Id.* at page 4, lines 14-16). Further, since small changes in nucleotides in gene sequences may result in reduced or enhanced activity of the gene product, the sequence with a small change may work as effectively as the full length gene. Also, since DNA sequences may include changes in certain codons, *i.e.*, wobble, that do not alter the amino acids of the polypeptide corresponding to the DNA sequences, one of skill in the art would expect the altered DNA sequences to correspond to an equivalent polypeptide as the un-altered DNA sequence.

In view of the amendments and remarks presented herein, reconsideration and withdrawal of the written description rejections are respectfully requested.

Rejections under 35 U.S.C. § 102

Claims 1-4, 6, 10-21 and 23

Claims 1-4, 6, 10-21 and 23 were rejected under 35 U.S.C. § 102(b) as assertedly being anticipated by Cahoon et al. (U.S. Patent 5,614,400). Applicants respectfully traverse the rejection as hereinafter set forth.

As amended, the claims require a nucleic acid corresponding to a polypeptide having diacylglycerol acyltransferase activity, wherein the nucleic acid includes a functional part of SEQ ID NO: 1 or 3. Thus, the functional part of SEQ ID NO: 1 or 3 corresponds to a polypeptide with diacylglycerol acyltransferase activity. Since Cahoon et al. does not disclose a polypeptide with diacylglycerol acyltransferase activity, Cahoon et al. does not anticipate the pending claims.

Reconsideration and withdrawal of the anticipation rejections of claims 1-4, 6, 10-21 and 23 are thus requested.

Claims 1-4

Claims 1-4 were further rejected under 35 U.S.C. § 102(b) as assertedly being anticipated by Newman et al. (Sept. 1997, NCBI Database, Accession number AA042298). Applicants respectfully traverse the rejections as hereinafter set forth.

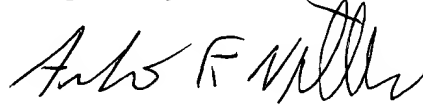
As amended, claims 1-4 require that the nucleic acid molecule corresponds to a polypeptide having diacylglycerol acyltransferase activity. The sequences of Newman et al. are not disclosed to correspond to a polypeptide having diacylglycerol acyltransferase activity. Further, when claims 1-4 are read in light of the specification, the sequences substantially homologous to SEQ ID NO: 1 and 3 are DNA sequences which correspond to proteins with deduced amino acid sequences of 25% or greater identity, and 40% or greater similarity when compared to SEQ ID NO: 1 or 3. (See, Specification at page 4, lines 14-16). Since the sequences disclosed in Newman et al. are only 17.7% identical and 2.7% identical with SEQ ID NO: 1 and 3, respectively, the sequences in Newman et al. do not anticipate claims 1-4.

Reconsideration and withdrawal of the anticipation rejections of claims 1-4 are thus respectfully requested.

CONCLUSION

In view of the foregoing amendments and remarks, the applicants respectfully submit that the claims define patentable subject matter. If any questions remain after consideration of the foregoing, the Office is kindly requested to contact applicants' attorney at the address or telephone number given herein.

Respectfully submitted,



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Enclosure: Copy of Deposit Receipt

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MARKED UP VERSION OF SPECIFICATION SHOWING CHANGES MADE

The inventors further used the partial cDNA sequence to search against *Arabidopsis thaliana* genomic sequence information. An *Arabidopsis* 'IGF' BAC clone 'F27F23' [[]accession no. AC 003058 []] was identified to include a region that matched the cDNA, and therefore it was concluded that this was the region encompassing the corresponding gene. Moreover, this BAC clone 'F27F23', is contained in the YAC clone, CIC06E08, which, according to the published map position [http://weeds.mgh.harvard.edu/goodman/c2_b.html], represents a region between centimorgan 35.9 and centimorgan 38.7 on chromosome II; this position is similar to the estimated location for *TAG1*, and the lesion identified by the mutation in AS11 (Katavic *et al.*, 1995). In view of our previous results on the characterization of the AS11 mutant, the map position of this gene strongly suggested that it may encode a DGAT.

MARKED UP VERSION OF CLAIMS SHOWING CHANGES MADE

1. (Amended) [Isolated] An isolated [and purified deoxyribonucleic] nucleic acid [(DNA)] molecule corresponding to a polypeptide having diacylglycerol acyltransferase activity, [characterized in that] wherein said [DNA] nucleic acid molecule includes a sequence according to SEQ ID NO: 1, [or] a functional part of SEQ ID NO: 1, or a sequence that is substantially homologous to SEQ ID NO: 1.

2. (Amended) [Isolated] An isolated [and purified deoxyribonucleic] nucleic acid [(DNA)] molecule corresponding to a polypeptide having diacylglycerol acyltransferase activity, [characterized in that] wherein said [DNA] nucleic acid molecule includes a sequence according to SEQ ID NO: 3, [or] a functional part of SEQ ID NO: 3, or a sequence that is substantially homologous to SEQ ID NO: 3.

3. (Amended) A vector for transformation of plant cells, [characterized in that] wherein said vector contains a [deoxyribonucleic] nucleic acid sequence corresponding to a polypeptide having diacylglycerol acyltransferase activity, wherein the sequence contains [according to] SEQ ID NO: 1, [or] contains a functional part of SEQ ID NO: 1, or contains a sequence that is substantially homologous to SEQ ID NO: 1.

4. (Amended) A vector for transformation of plant cells, [characterized in that] wherein said vector contains a [deoxyribonucleic] nucleic acid sequence corresponding to a polypeptide having diacylglycerol acyltransferase activity, wherein the sequence contains [according to] SEQ ID NO: 3, [or] contains a functional part of SEQ ID NO: 3, or contains a sequence that is substantially homologous to SEQ ID NO: 3.

5. (Twice amended) A vector for transformation of plant cells, [characterized in that] wherein said vector contains a [deoxyribonucleic] nucleic acid sequence according to SEQ ID NO: 23, which is SEQ ID NO: 1 altered to contain an 81 bp insertion, such that the deduced amino acid sequence of the encoded protein contains the repeated sequence [SHAGLFNLCVVVLI~~AVNSRLI~~ENLMK] SHAGLFNLCVVVLI~~AVNSRLI~~ENLMK according to SEQ ID NO: 25, where the spacing and identity of the [underlined amino acids] G at position 4, the N at position 7, the V at position 10, the V at position 11, the L at position 13, the I at position 14, the N at position 17, the R at position 19, the L at position 20, the E at position 23, the N at position 24, the L at position 25 and the K at position 27 are identical or are replaced by conserved substitutions.

6. (Twice amended) [A] The vector according to claim 3, [characterized in that] wherein said sequence is present in said vector in a sense orientation.

8. (Amended) Plasmid pDGATcDNA having accession number [(JATCC PTA-989[])].

9. (Amended) Plasmid pDGATgene having accession number [(JATCC PTA-988[])].

10. (Amended) A plant having a genome, [characterized in that] wherein the genome contains an introduced nucleotide sequence corresponding to a polypeptide having diacylglycerol acyltransferase activity, wherein the sequence is [of] SEQ ID NO: 1, [or a] an introduced functional part of SEQ ID NO: 1, or [a] an introduced sequence that is substantially homologous to SEQ ID NO: 1.

11. (Amended) A plant seed having a genome, [characterized in that] wherein said genome contains an introduced nucleotide sequence corresponding to a polypeptide having diacylglycerol acyltransferase activity, wherein the sequence is [of] SEQ ID NO: 1, [or a] an introduced functional part of SEQ ID NO: 1, or [a] an introduced sequence that is substantially homologous to SEQ ID NO: 1.

12. (Twice amended) A genetically transformed plant, [characterized in that] wherein said genome has been transformed by a vector according to claim 3 or claim 4.

13. (Twice amended) A genetically transformed plant seed, [characterized in that] wherein said seed has been transformed by a vector according to claim 3 or claim 4.

14. (Twice amended) [A] The plant seed [as claimed in] of Claim 11 [or Claim 13], [characterized by exhibiting] wherein the plant seed exhibits an altered oil seed oil content compared to an average of a statistically-significant number of seeds of [genomically-unmodified] untransformed plants of the same genotype grown in identical conditions at the same time.

15. (Twice amended) [A] The plant seed [as claimed in] of Claim 11 [or Claim 13], [characterized by exhibiting] wherein the plant seed exhibits an altered diacylglycerol content in its seed oil compared to an average of a statistically-significant number of seeds of [genomically-unmodified] untransformed plants of the same genotype grown in identical conditions at the same time.

16. (Twice amended) [A] The plant seed [as claimed in] of Claim 11 [or Claim 13], [characterized by exhibiting] wherein the plant seed exhibits a seed oil with an altered fatty acyl composition compared to an average of a statistically-significant number of seeds of a [genomically-unmodified] untransformed plant of the same genotype grown in identical conditions at the same time.

17. (Twice amended) [A] The plant [as claimed in] of Claim 10 [or Claim 12], [characterized by exhibiting] wherein the plant seed exhibits an enhanced biomass compared to an average of a statistically-significant number of genomically-unmodified plants of the same genotype grown in identical conditions at the same time.

18. (Twice amended) [A] The plant seed [as claimed in] of Claim 11 [or Claim 13], [characterized by exhibiting] wherein the plant seed exhibits an enhanced biomass compared to an average of a statistically-significant number of seeds of genomically-unmodified plants of the same genotype grown under identical conditions at the same time.

19. (Amended) A method of producing transgenic plants [by] comprising:
introducing a nucleotide sequence into a genome of [said] a plant[,];
[characterized in that] wherein said nucleotide sequence introduced into said genome corresponds to a polypeptide having diacylglycerol acyltransferase activity, wherein the sequence is [includes] SEQ ID NO: 1 or SEQ ID NO: 3, [or] a functional part of SEQ ID NO: 1 or SEQ ID NO: 3, or a sequence that is substantially homologous to SEQ ID NO: 1, [or to] SEQ ID NO: 3, [or] a part of SEQ ID NO: 1 or SEQ ID NO: 3.

20. (Amended) [A] The method according to claim 19, [characterized in that] wherein said plant is a member of the Brassicaceae.

21. (Amended) [A] The method according to claim 19, [characterized in that] wherein said plant is selected from the group consisting of *Arabidopsis thaliana*, borage (*Borago* spp.), Canola, castor (*Ricinus communis*), cocoa bean (*Theobroma cacao*), corn (*Zea mays*), cotton (*Gossypium* spp.), *Crambe* spp., *Cuphea* spp., flax (*Linum* spp.), *Lesquerella* and *Limnanthes* spp., Linola, nasturtium (*Tropaeolum* spp.), *Oenothera* spp., olive (*Olea* spp.), palm (*Elaeis* spp.), peanut (*Arachis* spp.), rapeseed, safflower (*Carthamus* spp.), soybean (*Glycine* and *Soja* spp.), sunflower (*Helianthus* spp.), tobacco (*Nicotiana* spp.), *Vernonia* spp., wheat (*Triticum* spp.), barley (*Hordeum* spp.), rice (*Oryza* spp.), oat (*Avena* spp.) sorghum (*Sorghum* spp.), rye (*Secale* spp.) and other members of the plant family Gramineae not listed.

23. (Twice amended) A method of changing the oil content, acyl composition or diacylglycerol/triacylglycerol [proportions] ratio of the seed oil of plant seeds [by] comprising:
introducing a [sense or anti-sense] nucleic acid construct comprising a nucleic acid sequence
corresponding to a polypeptide having diacylglycerol acyltransferase activity into a plant
transformation vector[,];
[using the vector to transform] transforming the genome of a plant or plant seed with the
vector[,];
expressing the nucleic acid sequence;
[and then] growing the plant or plant seed; and
extracting the oil from the plant seed[,];
[characterized in that] wherein said nucleic acid sequence is SEQ ID NO: 1, [or] SEQ ID NO: 3,
[or] a functional part of SEQ ID NO: 1 or SEQ ID NO: 3, or a sequence that is
substantially homologous to SEQ ID NO: 1 or SEQ ID NO: 3.